



OCT 10 2003

16

TECH CENTER 1000/2000

RAW SEQUENCE LISTING

DATE: 10/07/2003

PATENT APPLICATION: US/08/913,644

TIME: 13:59:02

Input Set : A:\19424PC Seq List.txt

Output Set: N:\CRF4\10072003\H913644.raw

4 <110> APPLICANT: Hofmann, Kathryn J.
 5 Jansen, Kathrin U.
 6 Neeper, Michael P.
 8 <120> TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE
 9 18
 11 <130> FILE REFERENCE: 19424PC
 13 <140> CURRENT APPLICATION NUMBER: 08/913,644
 > 14 <141> CURRENT FILING DATE: 1997-11-21
 16 <150> PRIOR APPLICATION NUMBER: PCT/US96/03649
 17 <151> PRIOR FILING DATE: 1996-03-18
 19 <150> PRIOR APPLICATION NUMBER: 08/408,669
 20 <151> PRIOR FILING DATE: 1995-03-22
 22 <150> PRIOR APPLICATION NUMBER: 08/409,122
 23 <151> PRIOR FILING DATE: 1995-03-22
 25 <160> NUMBER OF SEQ ID NOS: 16
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1524
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence
 37 <400> SEQUENCE: 1
 38 atggcctttgt ggcggcctag tgacaatacc gtataccttc cacctccttc tgtggcaaga 60
 39 gttgtaaata ctgatgatta tgtgactcgc acaagcatat tttatcatgc tggcagctct 120
 40 agattattaa ctgttggttaa tccatatttt agggttcctg cagggtggtg caataagcag 180
 41 gatattccta aggtttctgc ataccaatat agagtatttc ggggtgcagtt acctgaccca 240
 42 aataaatttg gtttacctga taatagtatt tataatcctg aaacacaacg tttagtgtgg 300
 43 gcctgtgctg gagtggaaat tggccgtggt cagcctttag gtggtggcct tagtgggcat 360
 44 ccattttata ataaattaga tgacactgaa agttcccatg ccgctacgtc taatgtttct 420
 45 gaggacgtta gggacaatgt gtctgtagat tataagcaga cacagttatg tattttgggc 480
 46 tgtgcccctg ctattgggga acactgggct aaaggcactg cttgtaaatc gcgtccttta 540
 47 tcacagggcg attgcccccc tttagaactt aagaacacag ttttggaaga tgggtgatag 600
 48 gtagatactg gatatggtgc catggacttt agtacattgc aagatactaa atgtgaggta 660
 49 ccattggata tttgtcagtc tatttgtaaa tatcctgatt atttacaaat gtctgcagat 720
 50 ccttatgggg attccatggt tttttgctta cgacgtgagc agctttttgc taggcatttt 780
 51 tggaataggg cagggtactat ggggtgacact gtgcctcaat ccttatatat taaaggcaca 840
 52 ggtatgcgtg cttcacctgg cagctgtgtg tattctccct ctccaagtgg ctctattggt 900
 53 acctctgact ccagttgtt taataaacca tattggttac ataaggcaca gggtcataac 960
 54 aatggtatct gctggcataa tcaattattt gttactgtgg tagataccac tcgtagtacc 1020
 55 aatttaacaa tatgtgcttc tacacagtct cctgtacctg ggcaatatga tgctaccaa 1080
 56 tttaagcagt atagcagaca tggtgaagaa tatgatttgc agtttatttt tcagttatgt 1140
 57 actattactt taactgcaga tggtatgtcc tatattcata gtatgaatag cagtatttta 1200

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58 gaggattgga acttttggtgt tcccccccg ccaactacta gtttggtgga tacatatcgt 1260
59 tttgtacaat ctgttgctat tacctgtcaa aaggatgctg caccagctga aaataaggat 1320
60 ccctatgata agttaaagtt ttggaatgtg gatttaaagg aaaagttttc tttggactta 1380
61 gatcaatata cccttgacg taaatttttg gttcaggctg gattgcgtcg caagcccacc 1440
62 ataggccctc gtaaacgttc tgcctcatct gccactacgt cttctaaacc tgccaagcgt 1500
63 gtgctgttac gtgccaggaa gtaa 1524

```

65 <210> SEQ ID NO: 2

66 <211> LENGTH: 507

67 <212> TYPE: PRT

68 <213> ORGANISM: Artificial Sequence

70 <220> FEATURE:

71 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence

73 <400> SEQUENCE: 2

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74 Met Ala Leu Trp Arg Pro Ser Asp Asn Thr Val Tyr Leu Pro Pro Pro
75 1 5 10 15
76 Ser Val Ala Arg Val Val Asn Thr Asp Asp Tyr Val Thr Arg Thr Ser
77 20 25 30
78 Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
79 35 40 45
80 Tyr Phe Arg Val Pro Ala Gly Gly Gly Asn Lys Gln Asp Ile Pro Lys
81 50 55 60
82 Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro
83 65 70 75 80
84 Asn Lys Phe Gly Leu Pro Asp Asn Ser Ile Tyr Asn Pro Glu Thr Gln
85 85 90 95
86 Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro
87 100 105 110
88 Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp
89 115 120 125
90 Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg
91 130 135 140
92 Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly
93 145 150 155 160
94 Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys
95 165 170 175
96 Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn
97 180 185 190
98 Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met
99 195 200 205
100 Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile
101 210 215 220
102 Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp
103 225 230 235 240
104 Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe
105 245 250 255
106 Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro
107 260 265 270
108 Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser
109 275 280 285

```

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```

110 Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser
111      290      295      300
112 Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn
113 305      310      315      320
114 Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr
115      325      330      335
116 Thr Arg Ser Thr Asn Leu Thr Ile Cys Ala Ser Thr Gln Ser Pro Val
117      340      345      350
118 Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val
119      355      360      365
120 Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu
121      370      375      380
122 Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu
123 385      390      395      400
124 Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Pro Thr Thr Ser Leu Val
125      405      410      415
126 Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp
127      420      425      430
128 Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp
129      435      440      445
130 Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro
131      450      455      460
132 Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr
133 465      470      475      480
134 Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys
135      485      490      495
136 Pro Ala Lys Arg Val Arg Val Arg Ala Arg Lys
137      500      505

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140 <210> SEQ ID NO: 3

141 <211> LENGTH: 1389

142 <212> TYPE: DNA

143 <213> ORGANISM: Artificial Sequence

145 <220> FEATURE:

146 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence

148 <400> SEQUENCE: 3

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149 atggtatccc accgtgccgc acgacgcaaa cgggcttcgg tgactgactt atataaaaca 60
150 tgtaaacaat ctggtacatg tccatctgat gttgttaata aggtagaggg caccacgtta 120
151 gcagataaaa tattgcaatg gtcaagcctt ggtatatttt tgggtggact tggcataggt 180
152 actggaagtg gtacaggggg tcgtacaggg tacattccat tgggtgggcg ttccaataca 240
153 gttgtggatg tcggtcctac acgtcctcca gtggttattg aacctgtggg cccacagac 300
154 ccatctattg ttacattaat agaggactca agtgttgtta catcaggtgc acctaggcct 360
155 acttttactg gcacgtctgg gtttgatata acatctgctg gtacaactac acctgcagtt 420
156 ttggatatca caccttcgtc tacctctgtt tctattttcca caaccaattt taccaatcct 480
157 gcattttctg atccgtccat tattgaagtt ccacaaactg gggaggtgtc aggtaatgta 540
158 tttgttggtg cccctacatc tggaacacat gggtatgaag aaataccttt acaaacattt 600
159 gcttcttctg gtacggggga ggaaccatt agtagtacc cattgcctac tgtgcggcgt 660
160 gtagcaggtc cccgccttta cagtagggcc taccaacaag tgtctgtggc taaccctgag 720
161 tttcttacac gtccatcctc tttaattacc tatgacaacc cggcctttga gcctgtggac 780
162 actacattaa catttgagcc tcgtagtaat gttcctgatt cagattttat ggatattatc 840

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```

163 cgtttacata ggcctgcttt aacatccagg cgtggtactg tgcgcttttag tagattaggt 900
164 caaagggcaa ctatgtttac ccgtagcggg acacaaatag gtgctagggt tcacttttat 960
165 catgatataa gtcctattgc accctcccca gaatatattg aactgcagcc tttagtatct 1020
166 gccacggagg acaatggctt gtttgatata tatgcagatg acatagaccc tgcaatgcct 1080
167 gtaccatcgc gtcctactac ctctctgca gtttctacat attcgccac tatatcatct 1140
168 gcctcttcct atagtaattg aacggtcctt ttaacctcct cttgggatgt gcctgtatac 1200
169 acgggtcctg atattacatt accacctact acctctgtat ggcccattgt atcacccaca 1260
170 gccctgcct ctacacagta tattggtata catggtacac attattattt gtggccatta 1320
171 tattatttta ttcctaaaaa gcgtaaacgt gttccctatt tttttgcaga tggctttgtg 1380
172 gcggcctag 1389

```

174 <210> SEQ ID NO: 4

175 <211> LENGTH: 461

176 <212> TYPE: PRT

177 <213> ORGANISM: Artificial Sequence

179 <220> FEATURE:

180 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence

182 <400> SEQUENCE: 4

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183 Met Val Ser His Arg Ala Ala Arg Arg Lys Arg Ala Ser Val Thr Asp
184 1 5 10 15
185 Leu Tyr Lys Thr Cys Lys Gln Ser Gly Thr Cys Pro Ser Asp Val Val
186 20 25 30
187 Asn Lys Val Glu Gly Thr Thr Leu Ala Asp Lys Ile Leu Gln Trp Ser
188 35 40 45
189 Ser Leu Gly Ile Phe Leu Gly Gly Leu Gly Ile Gly Thr Gly Ser Gly
190 50 55 60
191 Thr Gly Gly Arg Thr Gly Tyr Ile Pro Leu Gly Gly Arg Ser Asn Thr
192 65 70 75 80
193 Val Val Asp Val Gly Pro Thr Arg Pro Pro Val Val Ile Glu Pro Val
194 85 90 95
195 Gly Pro Thr Asp Pro Ser Ile Val Thr Leu Ile Glu Asp Ser Ser Val
196 100 105 110
197 Val Thr Ser Gly Ala Pro Arg Pro Thr Phe Thr Gly Thr Ser Gly Phe
198 115 120 125
199 Asp Ile Thr Ser Ala Gly Thr Thr Thr Pro Ala Val Leu Asp Ile Thr
200 130 135 140
201 Pro Ser Ser Thr Ser Val Ser Ile Ser Thr Thr Asn Phe Thr Asn Pro
202 145 150 155 160
203 Ala Phe Ser Asp Pro Ser Ile Ile Glu Val Pro Gln Thr Gly Glu Val
204 165 170 175
205 Ser Gly Asn Val Phe Val Gly Thr Pro Thr Ser Gly Thr His Gly Tyr
206 180 185 190
207 Glu Glu Ile Pro Leu Gln Thr Phe Ala Ser Ser Gly Thr Gly Glu Glu
208 195 200 205
209 Pro Ile Ser Ser Thr Pro Leu Pro Thr Val Arg Arg Val Ala Gly Pro
210 210 215 220
211 Arg Leu Tyr Ser Arg Ala Tyr Gln Gln Val Ser Val Ala Asn Pro Glu
212 225 230 235 240
213 Phe Leu Thr Arg Pro Ser Ser Leu Ile Thr Tyr Asp Asn Pro Ala Phe
214 245 250 255

```

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```

215 Glu Pro Val Asp Thr Thr Leu Thr Phe Glu Pro Arg Ser Asn Val Pro
216                               260                265                270
217 Asp Ser Asp Phe Met Asp Ile Ile Arg Leu His Arg Pro Ala Leu Thr
218                               275                280                285
219 Ser Arg Arg Gly Thr Val Arg Phe Ser Arg Leu Gly Gln Arg Ala Thr
220                               290                295                300
221 Met Phe Thr Arg Ser Gly Thr Gln Ile Gly Ala Arg Val His Phe Tyr
222 305                               310                315                320
223 His Asp Ile Ser Pro Ile Ala Pro Ser Pro Glu Tyr Ile Glu Leu Gln
224                               325                330                335
225 Pro Leu Val Ser Ala Thr Glu Asp Asn Gly Leu Phe Asp Ile Tyr Ala
226                               340                345                350
227 Asp Asp Ile Asp Pro Ala Met Pro Val Pro Ser Arg Pro Thr Thr Ser
228                               355                360                365
229 Ser Ala Val Ser Thr Tyr Ser Pro Thr Ile Ser Ser Ala Ser Ser Tyr
230                               370                375                380
231 Ser Asn Val Thr Val Pro Leu Thr Ser Ser Trp Asp Val Pro Val Tyr
232 385                               390                395                400
233 Thr Gly Pro Asp Ile Thr Leu Pro Pro Thr Ser Val Trp Pro Ile Val
234                               405                410                415
235 Ser Pro Thr Ala Pro Ala Ser Thr Gln Tyr Ile Gly Ile His Gly Thr
236                               420                425                430
237 His Tyr Tyr Leu Trp Pro Leu Tyr Tyr Phe Ile Pro Lys Lys Arg Lys
238                               435                440                445
239 Arg Val Pro Tyr Phe Phe Ala Asp Gly Phe Val Ala Ala
240                               450                455                460

```

243 <210> SEQ ID NO: 5

244 <211> LENGTH: 41

245 <212> TYPE: DNA

246 <213> ORGANISM: Artificial Sequence

248 <220> FEATURE:

249 <223> OTHER INFORMATION: oligonucleotide, sense primer

251 <400> SEQUENCE: 5

252 gaagatctca caaaacaaaa tggctttgtg gcggcctagt g

41

254 <210> SEQ ID NO: 6

255 <211> LENGTH: 36

256 <212> TYPE: DNA

257 <213> ORGANISM: Artificial Sequence

259 <220> FEATURE:

260 <223> OTHER INFORMATION: oligonucleotide, antisense primer

262 <400> SEQUENCE: 6

263 gaagatcttt acttcctggc acgtacacgc acacgc

36

265 <210> SEQ ID NO: 7

266 <211> LENGTH: 45

267 <212> TYPE: DNA

268 <213> ORGANISM: Artificial Sequence

270 <220> FEATURE:

271 <223> OTHER INFORMATION: oligonucleotide, sense primer

273 <400> SEQUENCE: 7

VERIFICATION SUMMARY

DATE: 10/07/2003

PATENT APPLICATION: US/08/913,644

TIME: 13:59:03

Input Set : A:\19424PC Seq List.txt

Output Set: N:\CRF4\10072003\H913644.raw

4 M:271 C: Current Filing Date differs, Replaced Current Filing Date